

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

08/986,606A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/986,606D

DATE: 08/09/2002

TIME: 13:48:47

Input Set : A:\SLOANE.txt

Output Set: N:\CRF4\08092002\H986606D.raw

ENTERED

4 <110> APPLICANT: Sloane, Nathan H  
 6 <120> TITLE OF INVENTION: Sixteen Amino Acid of the Antineoplastic Protein (ANUP)  
 7 as a Pharmaceutically Active Anti-Tumor Agent  
 9 <130> FILE REFERENCE: 99181  
 11 <140> CURRENT APPLICATION NUMBER: US 08/986,606D  
 13 <141> CURRENT FILING DATE: 1997-12-8  
 15 <160> NUMBER OF SEQ ID NOS: 1  
 17 <170> SOFTWARE: PatentIn ver. 2.0  
 19 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 16  
 23 <212> TYPE: PRT  
 25 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 29 <221> NAME/KEY: VARIANT  
 31 <222> LOCATION: (1)  
 33 <223> OTHER INFORMATION: Xaa is -N-Terminal pyroglutamyl (pyroGLU)  
 35 <223> OTHER INFORMATION: Description of Artificial Sequence, the partial N-terminal  
 36 amino acid sequence of the Antineoplastic Protein (ANUP)  
 W--> 38 <400> 1  
 W--> 40 Xaa Leu Lys Cys Tyr Thr Cys Lys Glu Pro Met Thr Ser Ala Ala Cys  
 41 1 5 10 15

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/986,606D

DATE: 08/09/2002  
TIME: 13:48:48

Input Set : A:\SLOANE.txt  
Output Set: N:\CRF4\08092002\H986606D.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1